PERSONAL INFORMATION

First Name/Surname	**ROBERTO PAGLIARINI**
Address	**DEPARTMENT OF MATHEMATICS, COMPUTER SCIENCE AND PHYSICS – UNIVERSITY OF UDINE - POLO SCIENTIFICO RIZZI, VIA DELLE SCIENZE 206, 33100, UDINE, ITALIA**
Telephone	**0432 553489**
E-mail	**roberto.pagliarini@uniud.it**
Nationality	Italian
Date of birth	23/07/1981

WORK EXPERIENCE

• Date (from – to)	February 2023 - Now
• University of Udine	Department of Mathematics, Computer Science and Physics
• Role	Assistant professor / University researcher
• Date (from – to)	July 2016 – February 2023
• IRCCS Ospedale San Raffaele	Genetics and Cell Biology Division
• Role	Senior Postdoctoral Fellow
	PI – Young Research Project, Italian Ministry of Health, Project Title: A Systems Biology Approach to Decipher the Complex Metabolic Changes in PolycysticKidney Disease: predicting the optimal 'cocktail' of combined diet/compounds for therapy
• Date (from – to)	June 2011 – June 2016
• Telethon Institute of Genetics and Medicine	Systems and Synthetic Biology Lab
• Role	Postdoctoral Fellow
• Date (from – to)	January 2011 – June 2011
• Università degli studi di Verona	Faculty of Mathematical, Physical, and Natural Science
• Role	Postdoctoral Fellow
• Date (from – to)	July 2009 – March 2010
• University of Cranfield	School of Health
• Role	Visiting Scientist

EDUCATION AND TRAINING

• Date (from - to)	January 2008 – December 2010
• University of Verona	School of Science, Engineering and Medicine
• Title of qualification awarded	Research Doctorate (PhD) in Computer Science – Doctoris Europaei
• Date (from - to)	Academic year 2006/2007
• University of Verona	Faculty of Mathematical, Physical, and Natural Science
•Title of qualification awarded	Master Degree in Computer Science

TEACHING ACTIVITIES

• Date	Academic year 2023/2024
• University of Udine	Master Degree in Molecular Biotechnologies
• Occupation or position held	Teacher of the course "Module III – Special Genetics and Bioinformatics"
• Date	Academic year 2023/2024
• University of Udine	Bachelor Degree in Biotechnology
• Occupation or position held	Teacher of the course "Graph Theory for Bioinformatics and System Biology" module of "Genome Analysis and Bioinformatics"
• Date	Academic year 2023/2024
• University of Udine	Bachelor Degree in Biotechnology
• Occupation or position held	Teacher of the course "Information Technology"
• Date	Academic year 2022/2023
• University of Udine	Bachelor Degree in Computer Science, Bachelor Degree in Internet of Things, Big Data, Machine Learning
• Occupation or position held	Teacher of the course "Algorithms and Data Structures and Laboratory"
• Date	Academic years 2016/2017, 2018/2019, 2019/2020, 2020/2021, 2021/2022
• Università Vita-Salute San Raffaele	Master Degree in Medicine and Surgery
• Occupation or position held	Teaching assistant of the course "Molecular Biology"
• Date	Academic year 2010/2011
• University of Verona	Bachelor Degree in Biotechnology
• Occupation or position held	Teaching assistant of the course "Computer Science"
• Date	Academic year 2010/2011
• University of Verona	Bachelor Degree in Applied Mathematics
• Occupation or position held	Teaching assistant of the course "Numerical Calculus"
• Date	Academic year 2008/2009
• University of Verona	Bachelor Degree in Applied Mathematics
• Occupation or position held	Teaching assistant of the course "Probability and Statistics"

MOTHER TONGUE	**ITALIAN**

ENGLISH

• Understanding	EXCELLENT
• Writing	EXCELLENT
• Speaking	GOOD

HONORS AND AWARDS

•"Post-Doctoral Fellowship-year 2018" award from Fondazione Umberto Veronesi for the year 2018.

•Bando ricerca finalizzata anno 2016 – Giovani Ricercatori (PI)" award from Italian Ministry of Health for the years 2018-2020.

SCIENTIFIC PUBBLICATIONS

Peer-reviewed Journal Papers

[1] M. Steidl, E. Nigro, A. Kallehauge Nielsen, R. Pagliarini, L. Cassina, M. Lampis, C. Podrini, M. Chiaravalli, V. Mannella, G. Distefano, M. Yang, M. Asnalayan, G. Musco, R. Roepman, C.Frezza, A. Boletta. Primary Cilia Sense Nutrient Availability and Respond to Glutamine via Asparagine Synthetase. Nature Metabolism, 5(3), pp. 385–397, 2023.

[2] R. Pagliarini, C. Podrini. Metabolic Reprogramming and Reconstruction: Integration of Experimental and Computational Studies to Set the Path Forward in ADPKD. Frontiers in Medicine, 8:740087, 2021.

[3] Podrini C.*, Rowe I.*, Pagliarini R.*, Costa A. S. H., Chiaravalli M., Di Meo I., Kim H., Distefano G., Tiranti V., Qian F., di Bernardo D., Frezza C., Boletta A. Dissection of Metabolic Reprogramming in Polycystic Kidney Disease Reveals a Complex and Coordinated Rewiring of Bioenergetic Pathways. Communications Biology, 1:194, 2018.

[4] L. Drusian., E.A. Nigro, V. Mannella., R. Pagliarini, M. Pema, A.S.H. Costa, F. Benigni.,A. Larcher, M. Chiaravalli, E. Gaude , F. Montorsi, U. Capitanio, G. Musco, C. Frezza, A. Boletta. mTORC1 Upregulation Leads to Accumulation of the Oncometabolite Fumarate in a Mouse Model of Renal Cell Carcinoma Cell Reports, 24 (5), pp. 1093-1104, 2018.

[5] R. Pagliarini, R. Castello, F. Napolitano, R. Borzone, P. Annunziata, G. Mandrile, M. De Marchi, N. Brunetti -Pierri, D. di Bernardo. In silico modelling of liver metabolism in a human disease reveals a key enzyme for histidiene and histamine homeostasis. Cell Reports, 15, 2292-2300, 2016.

[6] R. Pagliarini, R. Castello, R. Borzone, P. Annunziata, G. Mandrile, M. De Marchi, N. Brunetti -Pierri, D. di Bernardo. In-silico modelling of Primary Hyperoxaluria Type 1, a human inborn error of liver metabolism, unravels a key enzyme for histamine homeostasis. Inflammation Research, Volume 64, Supplement 1, 2015.

[7] R. Pagliarini, M. Sangiovanni, A. Peron, D. di Bernardo. Combining Flux Balance Analysis and Model Checking for Metabolic Network Validation and Analysis. Natural Computing, Natural Computing. Vol. 14, Issue 3, pp. 341 -354, 2015.

[8] V. Manca, A. Castellini, G. Franco, L. Marchetti, R. Pagliarini. Metabolic P Systems: A Discrete Model for Biological Dynamics. Chinese Journal of Electronics, Vol.22, No.4, 2013.

[9] R. Pagliarini, D. di Bernardo. A genome-scale modeling approach to study inborn errors of liver metabolism: toward an in silico patient . Journal of Computational Biology, 20(5), 2013.

[10] R. Pagliarini, O. Agrigoroaiei, G. Ciobanu, V. Manca. An Analysis of Correlative and Static Causality in P Systems. Lecture Notes in Computer Science, Volume 7762, pp 323-341, 2013.

[11] V. Manca, L. Marchetti, R. Pagliarini. MP Modelling of Glucose-Insulin Interactions in the Intravenous Glucose Tolerance Test. International Journal of Natural Computing Research, vol. 3, Issue2 , 2011 , pp. 13 -24

[12] G. Franco, V. Manca, R. Pagliarini. Regulation and Covering Problems in MP Systems. Lecture Notes in Computer Science, Volume 5957, pp. 242-251, 2010.

[13] A. Castellini, G. Franco and R. Pagliarini. Data analysis pipeline from laboratory to MP models. Natural Computing. Vol. 10, Issue 1, pp. 55-76, 2011.

[14] R. Pagliarini, G. Franco, V. Manca. An algorithm for initial fluxes of MP systems. International Journal of Computers, Communications & Control. Vol. IV, No. 3, pp. 263-272, 2009.

[15] V. Manca, R. Pagliarini, S. Zorzan. A photosynthetic process modelled by a metabolic P system. Natural Computing, Vol. 8, pp. 847-864, 2009.

[16] V. Manca, R. Pagliarini, S. Zorzan. Toward an MP model of Non Photochemical Quenching. Lecture Notes in Computer Science, volume 5391, pp. 299-310, 2009.

Refereed Conferences with Proceedings

[1] R. Pagliarini, F. Marroni, C. Piazza, G. Gabelli, G. Magris, G. Di Gaspero, M. Morgante, A. Policriti. Towards a Computational Approach to Quantification of Allele Specific Expression at Population Level. In 2nd edition of Workshop on Multi-Omics Data Integration for Modelling Biological Systems, MODIMO 2023.

[2] R. Pagliarini, A. Boletta. In SILICO Simulations Predict a Causative Link between Increased Glycolysis and Metabolic Reprogramming in Autosomal Dominant Polycystic Kidney Disease. In 16th IEEE Conference on Computational Intelligence in Bioinformatics and Computational Biology, CIBCB 2019.

[3] R. Pagliarini, L. Bianco, V. Manca, C. Bessant. Linking bistable dynamics to Metabolic P Systems. In Proceedings of the Eighth Brainstorming Week on Membrane Computing. Seville, Spain, February 2010.

[4] L. Bianco, R. Pagliarini, C. Bessant. Towards a GPU-aided simulation of nuclear receptors modulation. International Workshop on High Performance Computational Systems Biology, October 2009.

[5] R. Pagliarini, V. Manca. The discovery of initial fluxes of Metabolic P Systems. In Proceedings of the Seventh Brainstorming Week on Membrane Computing. Seville, Spain, February 2009.

Book Chapters

[1] G. Gambardella*, R. Pagliarini*, F. Gregoretti, G. Oliva, D. di Bernardo. Differential Equation Based Reverse-Engineering Algorithms: Pros and Cons. Gene Network Inference, Springer-Verlag Berlin Heidelberg, 2014.

[2] L. Marchetti, V. Manca, R. Pagliarini, A. Bolling-Fischer. MP Modelling for Systems Biology: two case studies. Applications of membrane computing in systems and synthetic biology. Applications of Membrane Computing in Systems and Synthetic Biology, volume 7 of Emergence, Complexity and Computation, pages 223 –245. Springer International Publishing, 2014.

Poster Papers, Abstracts and Posters

[1] R. Pagliarini, F. Marroni, C. Piazza, G. Gabelli, G. Magris, G. Di Gaspero, M. Morgante, A. Policriti. Towards a Computational Approach to Quantification of Allele Specific Expression at Population Level. In Workshop on Algorithms and Bioiformatics, WABI 2023, Houston, Texas, September 3-6, 2023.

[2] C. Podrini, I. Rowe, R. Pagliarini, S. Raineri, I. Di Meo, M. Chiaravalli, V. Tiranti, D. di Bernardo , A. Boletta. Global Profiling in Polycystic Kidney Disease Reveals a Metabolic Rewiring Reminiscent of Cancer. ASN Kidney Week 2016.

[3] R. Pagliarini, R. Castello, F. Napolitano, R. Borzone, P. Annunziata, G. Mandrile, M. De Marchi, N. Brunetti -Pierri, D. di Bernardo. A Computational Systems-Level Approach to Decipher Inborn Errors of Metabolism.13th Annual Meeting of the Bioinformatics Italian Society. University of Salerno, Italy, 15-17 June 2016.

[4] R. Pagliarini, R. Castello, N. Brunetti, D.di Bernardo. A Large-scale Computational Model of Inborn Error of Liver Metabolism Unravels Previously Unrecognized Metabolic Derangements and Novel Therapeutic Options. Sixth Annual RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges. Toronto, Canada, 2013.

[5] M. Sangiovanni, R. Pagliarini, D. di Bernardo, A. Peron. A Spin-based model checking approach for genome-scale metabolic networks validation and analysis. 4th International Workshop on Interactions between Computer Science and Biology. Florence, Italy, 2013.

[6] R. Pagliarini, D. di Bernardo. A genome-scale modelling approach to study inborn errors of liver metabolism: towards an in -silico patient. Fifth Annual RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges. San Francisco, USA, 2012.

[7] V. Manca, L. Marchetti, R. Pagliarini. Application of the MP theory for discovering biological models. 12th International Conference on Systems Biology. Mannheim Germany, 2011.

[8] R. Pagliarini, V. Manca. Inference of Biological Pathways by Integrating Different Kinds of Correlation Indexes. In Proceedings of XII International Congress on Molecular Systems Biology , Lleida, Spain , 8 -12 May 2011, pp. 102-102.

RESEARCH INTERESTS	• Natural Computing • Reverse Engineering of Biological Networks • Computational Biology • Systems Biology • Mathematical modelling of biological phenomena • Inborn Errors of Human Metabolism • Mathematical modelling of cancer metabolism
TALKS	•"Reverse engineering and modelling of metabolic networks: the case of Mendelian disorders"- 13th May 2014, BioPreDyn: The systems biology modeling cycle - building mechanistic dynamical models, EMBL-EBI, Hinxton, Cambridge, U. K., 12-15th May 2014. •"Computational Modelling of Inborn Errors of Liver Metabolism" - 19th June 2013, National Research Council (CNR), Naples, Italy. •"Systems biology of genetic diseases/integration of gene networks and metabolic networks" – 14th June 2013, BioPreDyn Workshop, Centre de Regulacio Genomica (CRG), Barcelona, Spain, 11-15th June 2013. •"Developing a mathematical modeling framework for linking signaling, regulation, and metabolism: metabolic processes under th e influence of hormones and genetic disorders as case studies" – 5th March 2013, 1st BioPreDyn Annual Metting, Naples, Italy, 4-6th March 2013. •"In silico simulations predict a causative link between increased glycolysis and metabolic reprogramming in autosomal dominant polycystic kidney disease." 16th IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology. Certosa di Pontignano, Italy, July 9-11, 2019. •"A Computational Systems-Level Approach to Decipher Inborn Errors of Metabolism." 13th Annual Meeting of the Bioinformatics Italian Society. University of Salerno, Italy, 15-17 June 2016. ▪"Differential Flux-balance Analysis: a new computational approach to identify alterations in human metabolic disorders" – 25th February 2015, BioPreDyn Annual Meeting 2015, Barcelona, Spain, 24 -25th February 2015. ▪"An analysis of correlative and quantitative causality in P systems" – 29th August 2013, CMC13 - The 13th International Conference on Membrane Computing, Budapest, Hungary, 28-31th August 2012. ▪"A genome-scale modelling approach to study inborn errors of liver metabolism: towards an in -silico patient" – 15th November 2012, Fifth Annual RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges. San Francisco, USA, 12-15th November 2012. ▪"Metabolic P Systems practical" – 9th February 2010, Cranfield University, Cranfield, U. K. ▪"Metabolic P Systems: an overview" -9th February 2010, Cranfield University, Cranfield, U. K. ▪"MP analysis of the stochastic Schlogel's reaction" – 4th February 2010, Eight Brainstorming Week on Membrane Computing, Sevilla, Spain 1-5th February 2010. ▪"MetaPlab, a virtual laboratory for Metabolic P systems: use examples and main structures" – 24th August 2009. Tenth Workshop on Membrane Computing, Curtea de Arges, Romania, 24-27th August 2009. ▪"Modelling and inferring biological phenomena by using Metabolic P Systems" – 24th April 2009. University of Verona, Department of Computer Science, Verona, Italy. ▪ "Multi-agent systems simulating the physiological role of plasmic membrane" – 22nd April 2009. University of Verona, Department of Computer Science, Verona, Italy. ▪"Log-Gain theory for Metabolic P systems: work in progress" – 19th March 2009. University of Verona, Department of Computer Science, Verona, Italy. ▪"Inferring the initial fluxes of a metabolic process" – 3rd February 2009, Seventh Brainstorming Week on membrane Computing, Sevilla, Spain 2-6th February 2009. ▪"Towards an MP model of non-photochemical quencing" – 20th July 2008. Ninth Workshop on Membrane Computing, Edinburgh, U.K., 29 - 31th July 2008. ▪"Quantum P Systems: Background, Definition and Computational Power" – 17th

September 2008. University of Verona, Department of Computer Science, Verona, Italy.

▪"The R language: what is it?" – 12th September 2008. University of Verona, Department of Computer Science , Verona, Italy.

▪"Reverse-engineering of gene networks" – 11th September 2008. University of Verona, Department of Computer Science, Verona, Italy.

PARTECIPATIONS IN CONGRESS AND CONFERENCES

Symbol * indicates conference talk.

•Workshop on Algorithms and Bioiformatics, WABI 2023, Houston, Texas, September 3-6, 2023.

•2nd edition of Workshop on Multi-Omics Data Integration for Modelling Biological Systems, MODIMO 2023, Birmingham 22 October 2023 *.

•DCGB Institutional Retreat, Brescia, Italy, 22-26th September, 2023 *.

•16th IEEE International Conference on Computational Intelligence in Bioinformatics and Computational Biology. Certosa di Pontignano, Italy, 9-11 July, 2019 *.

•13th Annual Meeting of the Bioinformatics Italian Society. University of Salerno, Italy, 15-17 June 2016, *.

•Sixth Annual RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challenges. Toronto, Canada, November 8-12, 2013 *.

•BioPreDyn Workshop, Centre de Regulacio Genomica (CRG), Barcelona, Spain, 11-15th June 2013 *.

•4th International Workshop on Interactions between Computer Science and Biology . Florence, Italy, 6th June 2013 *.

•1st BioPreDyn Annual Metting, Naples, Italy, 4-6th March 2013 *.

•Fifth Annual RECOMB/ISCB Conference on Regulatory and Systems Genomics, with DREAM Challen ges. San Francisco, USA, 12-15th November, 2012, *.

•The 13th International Conference on Membrane Computing, Budapest, Hungary, 28-31th August 2012 *.

•Tigem Institutional Retreat, Sorrento, Italy, 22-23th October, 2012.

•12th International Conference on Systems Biology, Mannheim, Germany, 28th August – 1st September 2011 *.

•XII International Congress on Molecular Systems Biology, Lleida, Spain, 8-12th May 2011 *.

•Eight Brainstorming Week on Membrane Computing, Sevilla, Spain, 1-5th February 2010 *.

•Tenth Workshop on Membrane Computing, Curtea de Arges, Romania, 24-27th August 2009 *.

•Seventh Brainstorming Week on Membrane Computing, Sevilla, Spain, 2-6th February 2009 *.

•The Architecture of Biological Complexity – Biocomplex 2008, Trento, Italy, 4-6th November 2008.

•Ninth Workshop on Membrane Computing, Edinburgh, U.K., 29-31th July 2008 *.

ACTIVITY AS REFEREE

• ACM Conference on Bioinformatics, Computational Biology, and Health Informatics.
• STAR Protocols, by Cell Press
• Review Editor of Optimization
• International Journal of Computers, Communications & Control
• IEEE International Conference on Bioinformatics & Biomedicine (BIBM)
• Gecco
• PPNS
• ECCB 2012
• ECCB 2016

Date, 26/11/2023